

TITLE: DSP-15 DUAL-SPECIFICITY PHOSPHATASE
Inventors: Ralf M. Luche et al. Docket No. 200125.433
EXPRESS MAIL NO. EL 897872305US

Figure 1

1 CCGGTGCCAG CCCAGGTGCT CGCGGCCTGG CTCCATGGCC CTGGTCACAG TGAGCCGTTT
61 GCGGCGGGC AGCGGCGCCT CCACGCCCCG GGGGCCCTGG GACCAGGCGG TCCAGCGAAG
121 GAGTCGACTC CAGCGAAGGC AGAGCTTTGC GGTGCTCCGT GGGGCTGTCC TGGGACTGCA
181 GGATGGAGGG GACAATGATG ATGCAGCAGA GGCCAGTTCT GAGCCAACAG AGAAGGCCCC
241 GAGTGAGGAG GAGCTCCACG GGGACCAGAC AGACTTCGGG CAAGGATCCC AGAGTCCCCA
301 GAAGCAGGAG GAGCAGAGGC AGCACCTGCA CCTCATGGTA CAGCTGCTGA GGCCGCAGGA
361 TGACATCCGC CTGGCAGCCC AGCTGGAGGC ACCCGGCCCT CCGCGGCTCC GCTACCTGCT
421 GGATGTTTCT ACACGAGAAG GAGAAGGTCT GAGCCAGGAT GAGACGGTCC TCCTGGGCGT
481 GGATTTCCCT GACAGCAGCT CCCCAGCTG CACCCTGGGC CTGGTCTTGC CCCTCTGGAG
541 TGACACCCAG GTGTACTTAG ATGGAGACGG GGGCTTCAGC GTGACGTCTG GTGGGCAAAG
601 CCGGATCTTC AAGCCCATCT CCATCCAGAC CATGTGGGCC AACTCCAGG TATTGCACCA
661 AGCATGTGAG GCAGCTCTAG GCAGCGGCCT TGTACCGGGT GGCAGTGCCC TCACCTGGGC
721 CAGCCACTAC CAGGAGAGAC TGAATCCGA ACAGAGCTGC CTCAATGAGT GGACGGCTAT
781 GGCCGACCTG GAGTCTCTGC GGCCTCCCAG CGCCGAGCCT GGCGGGTCCT CAGAACAGGA
841 GCAGATGGAG CAGGCGATCC GTGCTGAGCT GTGGAAAGTG TTGGATGTCA GTGACCTGGA
901 GAGTGTCACT TCCAAAGAGA TCCGCCAGGC TCTGGAGCTG CGCCTGGGGC TCCCCCTCCA
961 GCAGTACCGT GACTTCATCG ACAACCAGAT GCTGCTGCTG GTGGCACAGC GGGACCGAGC
1021 CTCCCGCATC TTCCCCCACC TCTACCTGGG CTCAGAGTGG AACGCAGCAA ACCTGGAGGA
1081 GCTGCAGAGG AACAGGGTCA CCCACATCTT GAACATGGCC CGGGAGATTG ACAACTTCTA
1141 CCCTGAGCGC TTCACCTACC ACAATGTGCG CCTCTGGGAT GAGGAGTCGG CCCAGCTGCT
1201 GCCGCACTGG AAGGAGACGC ACCGCTTCAT TGAGGCTGCA AGAGCACAGG GCACCCACGT
1261 GCTGGTCCAC TGCAAGATGG GCGTCAGCCG CTCAGCGGCC ACAGTGCTGG CCTATGCCAT
1321 GAAGCAGTAC GAATGCAGCC TGGAGCAGGC CCTGCGCCAC GTGCAGGAGC TCCGGCCCAT
1381 CGCCCGCCCC AACCCTGGCT TCCTGCGCCA GCTGCAGATC TACCAGGGCA TCCTGACGGC
1441 CAGCCGCCAG AGCCATGTCT GGGAGCAGAA AGTGGGTGGG GTCTCCCCAG AGGAGCAGCC
1501 AGCCCTGAA GTCTCTACAC CATTCCCACC TCTTCCGCCA GAACCTGAGG GTGGTGGGGA
1561 GGAGAAGGTT GTAGGCATGG AAGAGAGCCA GGCAGCCCCG AAAGAAGAGC CTGGGCCCAG
1621 GCCACGTATA AACCTCCGAG GGGTCATGAG GTCCATCAGT CTTCTGGAGC CCTCCTTGGA
1681 GCTGGAGAGC ACCTCAGAGA CCAGTGACAT GCCAGAGGTC TTCTCTTCCC ACGAGCTTTC
1741 ACATGAAGAG CCTCTGACG CCTTCCCACA GCTTGCAAGG ACCAAGGGAG GCCAGCAGGT
1801 GGACAGGGGG CCTCAGCCTG CCCTGAAGTC CCGCCAGTCA GTGGTTACCC TCCAGGGCAG
1861 TGCCGTGGTG GCCAACCAGA CCCAGGCCTT CCAGGAGCAG GAGCAGGGGC AGGGGCAGGG
1921 GCAGGGAGAG CCCTGCATTT CCTCTACGCC CAGGTTCCGG AAGGTGGTGA GACAGGCCAG
1981 CGTGCATGAC AGTGGAGAGG AGGGCGAGGC CTGAGCCCTC ACACATGCCC ACGCTCCCCT
2041 GACACTGAAG AGGATCCACA ACTCCTTGGA GAAACACCCT CACGTCTGTT GCCGCACACA
2101 TTCCTCTCAG CTCCGCCCCA TACCCGTCAC TACAGCCTCA CCTCCCACCC CTGTCACTAC
2161 GGCCTCACCT CCCACCCCTG TCACTACAGC CTCACCTCCT ACAGCCTTAA GTCCCAGGCC
2221 CATGTCTGCC TGTCCAAGGG CTCAAGACTT TCTAACTGGG ATGTGGTAGA GGGACTGAAG
2281 GTACCTTTGG GGGCAACAGC ACCCTAGTTT CATTCTCAAC TCTAGCCCTG CACTCTACC
2341 TGTGGCACGG AATGAAAACA GAGCTTCCCC TGCAAAAAGG GTCACGCCTC CCACCCCCGC
2401 CCCCTCCCTG CACCTCCTGT CCTCTCCAG TTCATTCTG GAACCAGCCA GGCCAGGCAA
2461 CAGTGGCCC CCAAAGGCAG GCAGGATCCT CAGGCCCCAG CCGCGGGAGG CTGGAAGGGC
2521 TGGCAGATCG CTTCCCTCAT CCACCTCCAC CGGTCCAGGT CTTTGCTGCT GTCCCAGAC
2581 CTCCTGTGAC ACCACGCCAG ATCACAGGGC ACCAGGCCAG AGATAGTCTT CTTTTTGTCC
2641 TTTCTGGCCT CTGGCTAGTC AGTTTTTCAT AGCCTTACAG TATCTGGCTT TGTACTGAGA
2701 AATAAAACAC ATTTTCAT

Figure **2**

MALVTVSRSPPGSGASTPVGPWDQAVQRRSRLQRRQSFAVLRGAVLGLQDGGDNDDAAEASSEPTKAPSEEEELHGD
QTDFGQGSQSPQKQEEQRQHLHLMVQLLRPQDDIRLAAQLEAPRPPRLRYLLVVSTREGEGLSQDETVLLGVDFPDS
SSPSC TLGLVLPLWSDTQVYLDGDGGFSVTSGGQSRI FKPI SIQTMWATLQVLHQACEAALGSGLVPGGSALTWASH
YQERLNSEQSCLNEW TAMADLES LRPPSAEPGGSSEQE QMEQAIRAE LWKVL DVSDLESVTSKEIRQAELRLGLPL
QQYRDFIDNQMLLLVAQRDRASRI FPHLYLGSEWNAANLEELQRNRVTHI LNMAREIDNFYPERFTYHNVRLWDEES
AQLLPHWKETHRFIEAARAQGTHVLVHCKMGVSRSAATVLAYAMKQYEC SLEQALRHVQELRPIARP NPGFLRQLQI
YQGILTASRQSHVWEQKVGGVSPEEHPAPEVSTPFPPLPPEPEGGEEKVVGMEESQAAPKEEPGPRPRINLRGVMR
SISLLEPSLELESTSETSDMPEVFSSHESSHEEPLQFPQLARTKGGQQVDRGPQPALKSRQSVVTLQGS AVVANRT
QAFQEQQEQGQGGQGEPCISSTPRFRKVVRQASVHDSGEEGEA

91	100	110	120	130	140	150	160	164	
1	+	+	+	+	+	+	+	+	
FIDEA-RGKNCGVL	VHCLAGISRSV	TYTYAYL	MQKLN	SLNDAYD	IYVKKKSN	ISPNFNF	HGQLD	FERTLGLS	
FIDEA-RSKKCGVL	VHCLAGISRSV	TYTYAYL	HQKHN	SLNDAYD	FYKRKKSN	ISPNFNF	HGQLD	FERTLGLS	
FIDEA-LSQNCGVL	VHCLAGISRSV	TYTYAYL	HQKHL	SLNDAYD	LVKRKKSN	ISPNFNF	HGQLD	FERTLGLS	
FIDKA-KLSSCQVI	VHCLAGISRSAT	IAIAYIM	KTHGMS	SDDAYR	FVKDRRPS	ISPNFNF	LGLLEYERTL	KLL	
FIDSV-KMSGGRVL	VHCQAGISRSAT	ICLAYL	IQSHRV	RLDEAFD	FVKQRRGI	ISPNFNF	SFMGQL	QLEQTQVLC	
FIDSI-KNAGGRV	FVHCQAGISRSAT	ICLAYL	MRTNRV	KLDEAFE	FVKQRRSI	ISPNFNF	SFMGQL	QFESQVLA	
YIDAV-KDCRGRVL	VHCQAGISRSAT	ICLAYL	MKKRV	RLDEAFE	FVKQRRSI	ISPNFNF	SFMGQL	QFESQVLA	
FIDCY-REKGGKVL	VHCEAGISRSPT	ICMAYL	MKTQFR	LKEAFD	IYKQRRSH	VSYPNF	FGFMGQL	LQYESEILPS	
FIDQALAQKNGRVL	VHCREGYSRSP	TLYIAYL	MHRQK	MDVKSAL	SIYRQNR	E-IGPNDG	FLAQLC	QLMDRLAKE	
FIEAA-RAQGTHVL	VHCKMGYSRSAT	YLAYAM	KQYEC	SLAQAL	RHVQEL	RPIARP	PNPGFL	RQLQIYQGIL	TAR
FI# a.....	VIYHC.aGISRSat	...AYIMsl..A...	ik..r..isPNF.F\$gQLI..#..I....					

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Figure 4

1 CCGGTGCCAG CCCAGGTGCT CGCGGCCTGG CTCCATGGCC CTGGTCACAG TGAGCCGTTC
61 GCGGGCGGGC AGCGGCGCCT CCACGCCCCT GGGGCCCTGG GACCAGGCGG TCCAGCGAAG
121 GAGTCGACTC CAGCGAAGGC AGAGCTTTGC GGTGCTCCGT GGGGCTGTCC TGGGACTGCA
181 GGATGGAGGG GACAATGATG ATGCAGCAGA GGCCAGTTCT GAGCCAACAG AGAAGGCCCC
241 GAGTGAGGAG GAGCTCCACG GGGACCAGAC AGACTTCGGG CAAGGATCCC AGAGTCCCCA
301 GAAGCAGGAG GAGCAGAGGC AGCACCTGCA CCTCATGGTA CAGCTGCTGA GGCCGCAGGA
361 TGACATCCGC CTGGCAGCCC AGCTGGAGGC ACCCGGGCCT CCGCGGCTCC GCTACCTGCT
421 GGTAGTTTCT ACACGAGAAG GAGAAGGTCT GAGCCAGGAT GAGACGGTCC TCCTGGGCGT
481 GGATTTCCCT GACAGCAGCT CCCCCAGCTG CACCCTGGGC CTGGTCTTGC CCCTCTGGAG
541 TGACACCCAG GTGTACTTAG ATGGAGACGG GGGCTTCAGC GTGACGTCTG GTGGGCAAAG
601 CCGGATCTTC AAGCCCATCT CCATCCAGAC CATGTGGGCC AACTCCAGG TATTGCACCA
661 AGCATGTGAG GCAGCTCTAG GCAGCGGCCT TGTACCGGGT GGCAGTGCCC TCACCTGGGC
721 CAGCCACTAC CAGGAGAGAC TGAATCCGA ACAGAGCTGC CTCAATGAGT GGACGGCTAT
781 GGCCGACCTG GAGTCTCTGC GGCTCCAG CGCCGAGCCT GGCGGGTCCT CAGAACAGGA
841 GCAGATGGAG CAGGCGATCC GTGCTGAGCT GTGGAAAGTG TTGGATGTCA GTGACCTGGA
901 GAGTGTCACT TCCAAAGAGA TCCGCCAGGC TCTGGAGCTG CGCTGGGGC TCCCCCTCCA
961 GCAGTACCGT GACTTCATCG ACAACCAGAT GCTGCTGCTG GTGGCACAGC GGGACCGAGC
1021 CTCCCGCATC TTCCCCACC TCTACCTGGG CTCAGAGTGG AACGCAGCAA ACCTGGAGGA
1081 GCTGCAGAGG AACAGGGTCA CCCACATCTT GAACATGGCC CGGGAGATTG ACAACTTCTA
1141 CCCTGAGCGC TTCACCTACC ACAATGTGCG CCTCTGGGAT GAGGAGTCGG CCCAGCTGCT
1201 GCCGCACTGG AAGGAGACGC ACCGCTTCAT TGAGGCTGCA AGAGCACAGG GCACCCACGT
1261 GCTGGTCCAC TGCAAGATGG GCGTCAGCCG CTCAGCGGCC ACAGTGCTGG CCTATGCCAT
1321 GAAGCAGTAC GAATGCAGCC TGGAGCAGGC CCTGCGCCAC GTGCAGGAGC TCCGGCCCAT
1381 CGCCCGCCCC AACCTGGCT TCCTGCGCCA GCTGCAGATC TACCAGGGCA TCCTGACGGC
1441 CAGAACCTGA GGGTGGTGGG GAGGAGAAGG TTGTAGGCAT GGAAGAGAGC CAGGCAGCCC
1501 CGAAAGAAGA GCCTGGGCCA CGGCCACGTA TAAACCTCCG AGGGGTCATG AGGTCCATCA
1561 GTCTTCTGGA GCCCTCCTTG GAGCTGGAGA GCACCTCAGA GACCAGTGAC ATGCCAGAGG
1621 TCTTCTCTTC CCACGAGTCT TCACATGAAG AGCCTCTGCA GCCCTTCCCA CAGCTTGCAA
1681 GGACCAAGGG AGGCCAGCAG GTGGACAGGG GGCCTCAGCC TGCCCTGAAG TCCCGCCAGT
1741 CAGTGGTTAC CCTCCAGGGC AGTGCCGTGG TGGCCAACCG GACCCAGGCC TTCCAGGAGC
1801 AGGAGCAGGG GCAGGGGCAG GGGCAGGGAG AGCCCTGCAT TTCCTCTACG CCCAGGTTCC
1861 GGAAGGTGGT GAGACAGGCC AGCGTGCATG ACAGTGGAGA GGAGGGCGAG GCCTGAGCCC
1921 TCACACATGC CCACGCTCCC CTGACACTGA AGAGGATCCA CAACTCCTTG GAGAAACACC
1981 CTCACGTCTG TTGCCGCACA CATTCTCTC AGCTCCGCCC CATACCCGTC ACTACAGCCT
2041 CACCTCCCAC CCCTGTCACT ACGGCCTCAC CTCCCACCCC TGTCACTACA GCCTCACCTC
2101 CTACAGCCTT AAGTCCCAGG CCCATGTCTG CCTGTCCAAG GGCTCAAGAC TTTCTAACTG
2161 GGATGTGGTA GAGGGACTGA AGGTACCTTT GGGGGCAACA GCACCCTAGT TTCATTCTCA
2221 ACTCTAGCCC TGCACACTCA CCTGTGGCAC GGAATGAAAA CAGAGCTTCC CGTGCAAAAA
2281 GGGTCACGCC TCCCACCCCC GCCCCCTCCC TGCACCTCCT GTCCTCTCCC AGTTCATTCC
2341 TGGAACCAGC CAGGCCAGGC AACCAGTGGC CCCCAGAGG AGGCAGGATC CTCAGGCCCC
2401 AGCCGCGGGA GGCTGGAAGG GCTGGCAGAT CGCTTCCCTC ATCCACCTCC ACCGGTCCAG
2461 GTCTTTGCTG CTGTCCCCAG ACCTCCTGTG ACACCACGCC AGATCACAGG GCACCAGGCC
2521 AGAGATAGTC TTCTTTTGT CTTTCTGGC CTCTGGCTAG TCAGTTTTTC ATAGCCTTAC
2581 AGTATCTGGC TTTGTACTGA GAAATAAAAC ACATTTTC

Figure 5

MALVTVSRSPPGSGASTPVGPWDQAVQRRSRLQRRQSFAVLRGAVLGLQDGGDNDDAAEASSEPTTEKAPSEEEELHGD
QTDFGQGSQSPQKQEEQRQHLLHLMVQLLRPQDDIRLAAQLEAPRPPRLRYLLVVSTREGEGLSQDETVLLGVDFPDS
SSPCTLGLVLPLWSDTQVYLDGDGGFSVTSGGQSRIFKPISIQTMWATLQVLHQACEAALGSGLVPGGSALTWASH
YQERLNSEQSCLNEWAMADLES LRPPSAEPGGSSEQEQMEQAIRAELWKVLDVSDLESVTSKEIRQALELRLGLPL
QQYRDFIDNQMLLLVAQRDRASRIFPHLYLGSEWNAANLEELQRNRVTHILNMAREIDNFYPERFTYHNVRLWDEES
AQLLPHWKETHRFIEAARAQGTHVLVHCKMGVSRSAATVLAYAMKQYECSEALRHVQELRPIARPNPGFLRQLQI
YQGILTART

[illegible]